EXHIBIT A

OFFICE OF CHIEF MEDICAL EXAMINER
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LABORATORY REPORT

SUSPECT: Dean Jones
NYSID NO: 08910184K
LAB NO: FBS14-00378
ARREST NO: B13641664
REPORT ID: CRT-0414-0529

RESULTS AND CONCLUSIONS:

PCR DNA typing using the AmpF/STR® Identifiler® PCR Amplification Kit was done on the buccal swab from Dean Jones. A DNA profile was determined.

This DNA profile was compared to the results in the following case:

FB Number	Complaint Number	Entity/Complainants	Case Report ID
FB13-04342	2012-046-12101	[redacted]	CRT-1213-0165

The results are consistent with those of Male Donor A. Based on the random match probability for unrelated individuals, Dean Jones **is the source** of the DNA found on the sample listed below.

- hat scrapings

Based on a comparison of the DNA profile of Dean Jones to the mixture found on the sample listed below, he cannot be ruled out as a contributor. Therefore, a likelihood ratio was calculated.

- glove swabs

The DNA mixture found on the glove swabs is approximately **1340 times more probable** if the sample originated from the Dean Jones and two unknown, unrelated persons than if it originated from three unknown, unrelated persons.

Therefore, there is very strong support that Dean Jones and two unknown, unrelated persons contributed to this mixture, rather than three unknown, unrelated persons.

This profile could not be compared to the results in the sample listed below due to an insufficient amount of DNA recovered from the evidence sample submitted.

- balaclava scrapings

The DNA profile of Dean Jones is suitable for entry into the OCME local DNA databank.

FBS14-00378 Dean Jones

EVIDENCE RECEIVED:

ITEM	VOUCHER	DATE RECEIVED	DESCRIPTION
1	2000304474	03/27/2014	buccal swab from Dean Jones

DISPOSITION:

The following items will be retained in the laboratory:

DNA extracts from samples and controls tested

The remainder of the evidence will be returned to the OCME Evidence Unit.

Analyst : Wing Wong
(Criminalist, Level II)
Administrative Review Date : 06/10/2014
Administrative Reviewer : Tracie Long

APPENDIX

General

This report has an associated Forensic Biology case file.

Background to DNA Testing

DNA (Deoxyribo-Nucleic Acid), the inherited genetic material found in cells, contains markers which can differ from person to person. **DNA testing** can determine these genetic markers and compare biological samples from different individuals.

Alternative forms of DNA markers are called **alleles**. Alleles are found at specific areas, or locations, of the DNA called **loci** (singular, **locus**).

STR (short tandem repeat) loci contain alleles with a variable number of short repeating segments.Each STR allele can be described using a number which represents its number of repeats. A **DNA profile** is the series of numbers describing the DNA alleles found at an individual's STR DNA loci.

DNA Testing

DNA testing involves several steps, including DNA extraction, DNA quantitation, PCR/DNA amplification, and analysis of the resulting DNA alleles.

DNA extraction recovers DNA from biological samples such as blood, bone, hair, saliva, semen, and skin cells.

Differential extraction is designed to physically separate the DNA in epithelial cells from the DNA in sperm cells, in samples which potentially contain a mixture of sperm and other cell types. As a result, separate "epithelial cell," "sperm cell," and "swab (or substrate) remains" DNA fractions are generated.Incomplete separation can occur and fractions may contain both sperm DNA and epithelial cell DNA.

DNA quantitation measures the amount of DNA extracted from samples by using a technique called quantitative real time polymerase chain reaction (qRT-PCR). If sufficient DNA is detected, DNA amplification and analysis can be attempted.

The **PCR** (polymerase chain reaction) technique produces large amounts of DNA from small starting amounts of DNA by repeated cycles of copying the DNA loci (**DNA amplification**); after amplification the alleles present in the sample are identified.

PCR DNA testing for STRs uses the **Applied Biosystems AmpF/STR® Identifiler® PCR Amplification Kit** with 28 amplification cycles (**Identifiler® 28**) or 31 amplification cycles (**Identifiler® 31**). Each STR locus tested in the Identifiler® Kit contains between 8 and 32 identifiable alleles. The **Applied Biosystems AmpF/STR Minifiler™ PCR Amplification Kit may also be used**. These Kits also test the Amelogenin locus, which is used to determine the sex origin of a sample.

Y-chromosome STRs (**Y-STR**) are male-specific STRs, not present in females, that are inherited from father to son, and should be identical for all male relatives of the paternal line. For example, brothers who share the same father will have the same Y-STR type. PCR DNA testing for Y-STRs uses the **Promega Power Y kit** or the **Applied Biosystems AmpF/STR Yfiler™ PCR Amplification** .

Conclusions for DNA Typing

Is the source of: The DNA profile of an individual matches an evidentiary DNA profile and the population frequency of the evidentiary DNA profile meets the threshold of 1 in greater than 6.80 trillion, assuming the source is not an identical twin.

Could be the source of: The DNA profile of an individual is consistent with an evidentiary DNA profile, and the population frequency of the evidentiary DNA profile does not meet the threshold of 1 in greater than 6.80 trillion unrelated people.

Is a major or minor contributor to the mixture: The DNA profile of an individual matches a major or minor evidentiary DNA profile determined from a mixture, and the DNA population frequency of the determined major or the minor DNA profile meets the threshold of 1 in greater than 6.80 trillion individuals, assuming that source is not an identical twin.

Could be a major or minor contributor to the mixture: The DNA profile of an individual is consistent with a major or minor evidentiary DNA profile determined from a mixture, and the DNA population frequency of the determined major or the minor DNA profile does not meet the threshold of 1 in greater than 6.80 trillion unrelated people.

Could be a contributor to the mixture: For mixtures where individual profiles were not determined, all of the DNA alleles seen in an individual's DNA profile were also seen in the mixture for the locations where comparisons could be made.

Cannot be excluded as a contributor to the mixture: For the locations where comparisons could be made, most of the DNA alleles seen in an individual's DNA profile were also seen in the mixture. The allele(s) that were absent could be explained by any of several factors. Therefore, this person cannot be ruled out as a possible contributor to the mixture.

Excluded as a contributor to the mixture: For the locations where comparisons could be made, one or more of the DNA alleles seen in an individual's DNA profile were not seen in the mixture and this absence cannot be explained. Therefore, this person can be ruled out as a contributor.

No conclusions can be drawn: The results do not support a positive association or an exclusion. Therefore, it cannot be determined whether a person can or cannot be excluded to the mixture.

Not suitable for comparison: The DNA results on the evidence are either too incomplete or too complex to be the basis for conclusions regarding the source of the DNA.

Partial Match: An association between two single-source (clean or fully deconvoluted) profiles, showing similarities but short of an exact match, that suggests that the source of a profile is potentially a relative of the source of the other, partially matching, profile. Partial matches are inadvertent, and may be found at the local, state, or national levels (through comparison at the bench, LINKAGE, or CODIS searches).

Likelihood ratios:
For some mixtures wherein an individual contributor's DNA profile cannot be determined, a known person's DNA profile can still be compared to the mixture. The comparison DNA profile can be from a known person, or from a single source or deduced profile from within a case. For these comparisons, a statistical value known as a likelihood ratio (LR) may be calculated. The LR value provides a statistical measurement of the strength of support for one scenario over another, i.e., one scenario being that the known person contributed to the mixture versus the scenario that an unknown, unrelated person contributed instead.

Limited, moderate, strong or very strong support: These terms describe the strength or weakness of different ranges of a likelihood ratio (as shown in the table below). Examples of factors that affect the LR value include the amount of DNA tested, the type of mixture (for example, the number of contributors), instances when one or more of the individual's DNA alleles are not seen in the mixture, the presence of rare alleles in the mixture, and the presence of extra DNA alleles in the mixture.

Reported value	Qualitative interpretation
1	No conclusions
1 to 10	Limited support
10 to 100	Moderate support
100 to 1000	Strong support
Greater than 1000	Very strong support

Note, if the LR value is less than one, this means that the mixture is better explained if an unknown, unrelated person contributed to the mixture rather than the known person. This situation is reported as 1/LR and the qualitative terms from the table above are applied.

CODIS

The COmbined DNA Index System administered by the FBI. CODIS links DNA evidence obtained from crime scenes, thereby identifying serial criminals. CODIS also compares crime scene evidence to DNA profiles obtained from offenders, thereby providing investigators with the identity of the putative perpetrator. In addition, CODIS contains profiles from missing persons, unidentified human remains and relatives of missing persons.

There are three levels of CODIS: the Local DNA Index System (LDIS), used by individual laboratories; the State DNA Index System (SDIS),used at the state level to serve as a state's DNA database containing DNA profiles from LDIS laboratories; and the National DNA Index System (NDIS), managed by the FBI as the nation's DNA database containing all DNA profiles uploaded by participating states.